

Serial Number: 09/786,043

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/786,043

DATE: 10/16/2001

TIME: 17:52:08

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10162001\I786043.raw

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6   Zhou, Jiong
8 <120> TITLE OF INVENTION: Novel Therapeutic Molecules and Uses Therefor
10 <130> FILE REFERENCE: DAVI121.001APC
12 <140> CURRENT APPLICATION NUMBER: 09/786,043
13 <141> CURRENT FILING DATE: 2001-2-27
15 <150> PRIOR APPLICATION NUMBER: PCT/AU99/00691
17 <151> PRIOR FILING DATE: 1999-08-26
19 <150> PRIOR APPLICATION NUMBER: AU PP5512
21 <151> PRIOR FILING DATE: 1998-08-27
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn Ver. 2.0
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40                                     Met Leu Asp
41                                     1
43 tgc gtg aca cac agc acc ttc ctg cct aat gca tcc ttc tgc gat ccc 166
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48 Leu Met Ser Trp Thr Asp Leu Phe Ser Asn Glu Glu Tyr Tyr Pro Ala
49 20               25               30               35
51 ttt gag cat cag aca gcc tgt gac tca tac tgg aca tca gtc cac cct 262
52 Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser Val His Pro
53               40               45               50
55 gaa tac tgg act aag cgc cat gtg tgg gag tgg ctc cag ttc tgc tgc 310
56 Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln Phe Cys Cys
57   55               60               65
59 gac cag tac aag ttg gac acc aat tgc atc tcc ttc tgc aac ttc aac 358
60 Asp Gln Tyr Lys Leu Asp Thr Asn Cys Ile Ser Phe Cys Asn Phe Asn
61   70               75               80
63 atc agt ggc ctg cag ctg tgc agc atg aca cag gag gag ttc gtc gag 406
64 Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu Phe Val Glu
65   85               90               95
67 gca gct ggc ctc tgc ggc gag tac ctg tac ttc atc ctc cag aac atc 454
68 Ala Ala Gly Leu Cys Gly Glu Tyr Leu Tyr Phe Ile Leu Gln Asn Ile
69 100               105               110               115
71 cgc aca caa ggt tac tcc ttt ttt aat gac gct gaa gaa agc aag gcc 502
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79 aaa agt caa gac tgt cac agt cat agt aga aca agc ctc caa agt tct 598
80 Lys Ser Gln Asp Cys His Ser His Ser Arg Thr Ser Leu Gln Ser Ser
81          150          155          160
83 cat cta tgg gaa ttt gta cga gac ctg ctt cta tct cct gaa gaa aac 646
84 His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser Pro Glu Glu Asn
85          165          170          175
87 tgt ggc att ctg gaa tgg gaa gat agg gaa caa gga att ttt cgg gtg 694
88 Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile Phe Arg Val
89 180          185          190          195
91 gtt aaa tcg gaa gcc ctg gca aag atg tgg gga caa agg aag aaa aat 742
92 Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln Arg Lys Lys Asn
93          200          205          210
95 gac aga atg aca tat gaa aag ttg agc aga gcc ctg aga tac tac tat 790
96 Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr
97          215          220          225
99 aaa aca gga att ttg gag cgg gtt gac cga agg tta gtg tac aaa ttt 838
100 Lys Thr Gly Ile Leu Glu Arg Val Asp Arg Arg Leu Val Tyr Lys Phe
101          230          235          240
103 gga aaa aat gca cac ggg tgg cag gaa gac aag cta tgatctgctc 884
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121 Tyr Pro Ala Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser
122 35 40 45
124 Val His Pro Glu Tyr Trp Thr Lys Arg His Val Trp Glu Trp Leu Gln
125 50 55 60
127 Phe Cys Cys Asp Gln Tyr Lys Leu Asp Thr Asn Cys Ile Ser Phe Cys
128 65 70 75 80
130 Asn Phe Asn Ile Ser Gly Leu Gln Leu Cys Ser Met Thr Gln Glu Glu
131 85 90 95
133 Phe Val Glu Ala Ala Gly Leu Cys Gly Glu Tyr Leu Tyr Phe Ile Leu
134 100 105 110
136 Gln Asn Ile Arg Thr Gln Gly Tyr Ser Phe Phe Asn Asp Ala Glu Glu
137 115 120 125
139 Ser Lys Ala Thr Ile Lys Asp Tyr Ala Asp Ser Asn Cys Leu Lys Thr
140 130 135 140

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148 Glu Glu Asn Cys Gly Ile Leu Glu Trp Glu Asp Arg Glu Gln Gly Ile
149                               180                               185                               190
151 Phe Arg Val Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln Arg
152                               195                               200                               205
154 Lys Lys Asn Asp Arg Met Thr Tyr Glu Lys Leu Ser Arg Ala Leu Arg
155                               210                               215                               220
157 Tyr Tyr Tyr Lys Thr Gly Ile Leu Glu Arg Val Asp Arg Arg Leu Val
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177 tgccctcacg gta atg ttg gac tcg gtg aca cac agc acc ttc ctg cct 169
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179                               1                               5                               10
181 aat gca tcc ctc tgc gat ccc ctg atg tcg tgg act gat ctg ttc agc 217
182 Asn Ala Ser Leu Cys Asp Pro Leu Met Ser Trp Thr Asp Leu Phe Ser
183                               15                               20                               25
185 aat gaa gag tac tac cct gcc ttt gag cat cag aca gat gct gat tcc 265
186 Asn Glu Glu Tyr Tyr Pro Ala Phe Glu His Gln Thr Asp Ala Asp Ser
187                               30                               35                               40
189 aac tgc ttg aaa aca agt ggc atc aaa agc caa gac tgt cac agt cat 313
190 Asn Cys Leu Lys Thr Ser Gly Ile Lys Ser Gln Asp Cys His Ser His
191 45                               50                               55                               60
193 agt aga aca agc ctc caa agt tct cat cta tgg gaa ttt gta cga gac 361
194 Ser Arg Thr Ser Leu Gln Ser Ser His Leu Trp Glu Phe Val Arg Asp
195                               65                               70                               75
197 ctg ctt cta tct cct gaa gaa aac tgt ggc att ctg gaa tgg gaa gat 409
198 Leu Leu Leu Ser Pro Glu Glu Asn Cys Gly Ile Leu Glu Trp Glu Asp
199                               80                               85                               90
201 agg gaa caa gga att ttt cgg gtg gtt aaa tcg gaa gcc ctg gca aag 457
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203                               95                               100                               105
205 atg tgg gga caa agg aag aaa aat gac aga atg aca tat gaa aag ttg 505
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234 Tyr Pro Ala Phe Glu His Gln Thr Asp Ala Asp Ser Asn Cys Leu Lys
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237 Thr Ser Gly Ile Lys Ser Gln Asp Cys His Ser His Ser Arg Thr Ser
238          50          55          60
240 Leu Gln Ser Ser His Leu Trp Glu Phe Val Arg Asp Leu Leu Leu Ser
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244          85          90          95
246 Ile Phe Arg Val Val Lys Ser Glu Ala Leu Ala Lys Met Trp Gly Gln
247          100          105          110
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250          115          120          125
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270 tggactccgt aaccatagc accttctgc ccaacgcac cttctgtgac cccctgatgc 180
272 cttggaccga tctgttcagc aatgaagact actaccctgc ctttgagcat cagacagcct 240
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356 Met
357 1
358 ttg gac tcc gta acc cat agc acc ttc ctg ccc aac gca tcc ttc tgt 167
359 Leu Asp Ser Val Thr His Ser Thr Phe Leu Pro Asn Ala Ser Phe Cys
360 5 10 15
362 gac ccc ctg atg cct tgg acc gat ctg ttc agc aat gaa gac tac tac 215
363 Asp Pro Leu Met Pro Trp Thr Asp Leu Phe Ser Asn Glu Asp Tyr Tyr
364 20 25 30
366 cct gcc ttt gag cat cag aca gcc tgt gat tcc tac tgg aca tca gtg 263
367 Pro Ala Phe Glu His Gln Thr Ala Cys Asp Ser Tyr Trp Thr Ser Val
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370 cac cct gaa tac tgg acc aag cgc cat gtc tgg gaa tgg ctc caa ttc 311

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VERIFICATION SUMMARY

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